

CLAIMS:

1. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:
 - (i) the nucleic acid sequence depicted in any one of SEQ ID NO: 1 to
5 SEQ ID NO:48611 (denoted as NV_1 to NV_48611 on the CD-ROM);
 - (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
 - 10 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.
2. An isolated nucleic acid sequence complementary to the nucleic acid
15 sequence of Claim 1.
3. An amino acid sequence selected from the group consisting of:
 - (i) an amino acid sequence coded by the isolated nucleic acid sequence of alternative splice variants of Claim 1;
 - (ii) homologues of the amino acid sequences of (i) in which one or more
20 amino acids has been added, deleted, replaced or chemically modified in the region, or adjacent to the region, where the amino acid sequences differs from the original amino acid sequence, coded by the original nucleic acid sequence from which the variant has been varied by alternative splicing; and
 - (iii) amino acid sequences appearing on the CD-ROM.
- 25 4. An isolated nucleic acid sequence coding for any one of the amino acid sequences of Claim 3.
5. A purified antibody which binds specifically to any of the amino acid sequence of Claim 3.

00224675-12300

6. A purified antibody which binds to an amino acid sequence which is present only in the alternative splice variant depicted in the amino acid of Claim 3, but is not present in the original amino sequence.
7. A purified antibody which binds to an amino acid sequence present in the original amino acid sequence, which amino acid sequence is not present in the amino acid sequence of Claim 3.
8. An expression vector comprising any one of the nucleic acid sequences of Claim 1 and control elements for the expression of the nucleic acid sequence in a suitable host.
9. An expression vector comprising any one of the nucleic acid sequences of Claim 2, and control elements for the expression of the nucleic acid sequences in a suitable host.
10. A host cell transfected by the expression vector of Claim 8.
11. A host cell transfected by the expression vector of Claim 9.
12. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and as an active ingredient an agent selected from the group consisting of:
 - (i) the expression vector of Claim 8; and
 - (ii) any one of the amino acid sequences of Claim 3.
13. A pharmaceutical composition according to Claim 12, for treatment of diseases which can be ameliorated or cured by raising the level of any one of the amino acid sequences of Claim 3.
14. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and as an active ingredient an agent selected from the group consisting of:
 - (i) any one of the nucleic acid sequences of Claim 2;
 - (ii) the expression vector of Claim 9; and
 - (iii) the purified antibody of Claim 5.
15. A pharmaceutical composition according to Claim 14, for treatment of diseases which can be ameliorated or cured by decreasing the level of any one of the amino acid sequences of Claim 3.

16. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV_1-5525;
- (ii) nucleic acid sequences having at least 90% identity with the
5 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in
10 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

17. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV_5526-6579;
- 15 (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment
20 contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

18. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- 25 (i) the nucleic acid sequence depicted in any one of NV_6580-6781;
- (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

00321 94260

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

5 19. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV_6782-7426;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original
10 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been
15 varied by alternative splicing.

20 20. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV_7427-10085;

(ii) nucleic acid sequences having at least 90% identity with the
20 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in
25 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

21. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV_10086-10386;

00827 94260

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

- 5 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

22. An isolated nucleic acid sequence, of an alternative splicing variant, selected
10 from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV_10387-10762;
(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by
15 alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

20 23. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV_10763-11439;
(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original
25 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been
30 varied by alternative splicing.

003217 92942760

24. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (a) the nucleic acid sequence depicted in any one of NV_11440-11463;
- (b) nucleic acid sequences having at least 90% identity with the
5 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (c) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in
10 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

25. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV_11464-11572;
- 15 (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment
20 contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

26. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- 25 (i) the nucleic acid sequence depicted in any one of NV_11573-11599;
- (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

00924636-1800

27. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

(i) the nucleic acid sequence depicted in any one of NV_12506-12648;

(ii) nucleic acid sequences having at least 90% identity with the

20 sequence of (i) with the proviso that each sequence is different than the original
nucleic acid sequence from which the sequences of (i) have been varied by
alternative splicing; and

29. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV 12649-13504;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

5 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

30. An isolated nucleic acid sequence, of an alternative splicing variant, selected
10 from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV_1350-5-14159;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by
15 alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

20 31. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV_14160-14368;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original
25 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been
30 varied by alternative splicing.

09724676 112800

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

5 35. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV_15896-17110;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original
10 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been
15 varied by alternative splicing.

36. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV_17111-18639;

(ii) nucleic acid sequences having at least 90% identity with the
20 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in
25 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

37. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV_18640-19766;

09724676-112800

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

- 5 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

38. An isolated nucleic acid sequence, of an alternative splicing variant, selected
10 from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV_19767-22843;
(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by
15 alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

20 39. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV_22844-23081;
(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original
25 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been
30 varied by alternative splicing.

00821 9294260

40. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV_23082-27305;
- (ii) nucleic acid sequences having at least 90% identity with the
5 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment
10 contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

41. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV_27306-29408;
- 15 (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment
20 contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

42. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- 25 (i) the nucleic acid sequence depicted in any one of NV_29409-29485;
- (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

00321 9294260

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

5 **43.** An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

 (i) the nucleic acid sequence depicted in any one of NV_29486-29914;

 (ii) nucleic acid sequences having at least 90% identity with the
sequence of (i) with the proviso that each sequence is different than the original
10 nucleic acid sequence from which the sequences of (i) have been varied by
alternative splicing; and

 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment
contains a sequence which is not present, as a continuous stretch of nucleotides, in
the original nucleic acid sequence from which the sequences of (i) have been
15 varied by alternative splicing.

44. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

 (i) the nucleic acid sequence depicted in any one of NV_29915-30434;

 (ii) nucleic acid sequences having at least 90% identity with the
20 sequence of (i) with the proviso that each sequence is different than the original
nucleic acid sequence from which the sequences of (i) have been varied by
alternative splicing; and

 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment
contains a sequence which is not present, as a continuous stretch of nucleotides, in
25 the original nucleic acid sequence from which the sequences of (i) have been
varied by alternative splicing.

45. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

 (i) the nucleic acid sequence depicted in any one of NV_30435-30575;

003217 92942600

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

- 5 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

46. An isolated nucleic acid sequence, of an alternative splicing variant, selected
10 from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV_30576-31459;
(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by
15 alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

20 47. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV_31460-31753;
(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original
25 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been
30 varied by alternative splicing.

00821 9294260

48. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV_31754-33145;
- (ii) nucleic acid sequences having at least 90% identity with the
5 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in
10 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

49. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV_33146-34829;
- 15 (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment
20 contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

50. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- 25 (i) the nucleic acid sequence depicted in any one of NV_34830-35550;
- (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

00321" 9254260

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

5 **51.** An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV_35551-35660;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original
10 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been
15 varied by alternative splicing.

52. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV_35661-36150;

(ii) nucleic acid sequences having at least 90% identity with the
20 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in
25 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

53. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV_36151-37125;

00221 929260

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

5 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

54. An isolated nucleic acid sequence, of an alternative splicing variant, selected
10 from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV_37126-38380;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by
15 alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

20 55. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV_38381-45130;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original
25 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been
30 varied by alternative splicing.

00827 92942760

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

5 **59.** A method for detecting a variant nucleic acid sequence in a biological sample, comprising the steps of:

(b) detecting said hybridization complex;

(a) hybridizing to nucleic acid material of said biological sample any one nucleic acid sequences of Claim 1; and

(b) determining the amount of hybridization complexes and normalizing

20 (a) determining the level of the variant nucleic acid sequence in the first biological sample according to the method of Claim 60;

(c) comprising the levels obtained in (a) and (b) to give said ratio.

63. A method according to Claim 59, wherein the nucleic acid material of said biological sample are mRNA transcripts.

64. A method according to Claim 59, where the nucleic acid sequence is present
30 in a nucleic acid chip.

65. A method for detecting any one of the amino acid sequences of Claim 3 in a biological sample, comprising the steps of:

(a) contacting with said biological sample the antibody of Claim 5, thereby forming an antibody-antigen complex; and

5 (b) detecting said antibody-antigen complex

wherein the presence of said antibody-antigen complex correlates with the presence of the desired amino acid in said biological sample.

66. A method for detecting the level of the amino acid sequence of any one of Claim 3 in a biological sample, comprising the steps of:

10 (a) contacting with said biological sample the antibody of Claim 5, thereby forming an antibody-antigen complex; and

(b) detecting the amount of said antibody-antigen complex and normalizing said amount to provide the level of said amino acid sequence in the sample.

15 67. A method for determining the ratio between the level of any one of the amino acid sequence of Claim 3 present in a first biological sample and the level of the original amino acid sequences from which they were varied by alternative splicing, present in a second biological sample, the method comprising:

(a) determining the level of the amino acid sequences of Claim 3 into a
20 first sample by the method of Claim 66;

(b) determining the level of the original amino acid sequence in the second sample; and

(c) comparing the level obtained in (a) and (b) to give said ratio.

25 68. A method according to Claim 67, wherein said first and said second biological samples are the same sample.

69. A nucleic acid sequence according to Claim 1, present on a data carrier.

70. A data carrier comprising substantially all the nucleic acid sequences depicted in NV_1 to NV_48611.

30 71. A data carrier according to Claim 70, further comprising the amino acid sequences coded by any one of NV_1 to NV_48611.

00321 9294260

72. A data carrier according to Claim 71, for use in an analysis of a nucleic acid sequence in which said nucleic acid sequence is compared to any of the sequence present on the data carrier.

73. A software data combination comprising:

- 5 a nucleic acid sequence search and comparison software and data comprising substantially sequences depicted in NV_1 to NV_48611; said combination when loaded into a computer can execute in the computer a search where a nucleotide sequence is compared to the sequences comprising said data.

00827 9294260